

S. Kaushal

1633

ENTERED

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/155,327B

DATE: 05/31/2000
 TIME: 13:59:31

Input Set : A:\11686.seq2
 Output Set: N:\CRF3\05312000\I155327B.raw

3 <110> APPLICANT: AMRAD Operations Pty Ltd
 5 <120> TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
 6 FAMILY OF APOPTOSIS-CONTROLLING GENES
 8 <130> FILE REFERENCE: 2096584
 10 <140> CURRENT APPLICATION NUMBER: 09/155,327B
 C--> 11 <141> CURRENT FILING DATE: 1999-03-29
 13 <150> PRIOR APPLICATION NUMBER: PN8965
 14 <151> PRIOR FILING DATE: 1996-03-27
 16 <160> NUMBER OF SEQ ID NOS: 9
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 33
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Mouse
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 26 <221> NAME/KEY: modified_base /
 27 <222> LOCATION: 16
 28 <223> OTHER INFORMATION: n is inosine
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 32 <222> LOCATION: 19
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 42 <222> LOCATION: 25
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 50 <211> LENGTH: 9
 51 <212> TYPE: PRT
 52 <213> ORGANISM: Mouse
 54 <220> FEATURE:
 55 <221> NAME/KEY: Unsure
 56 <222> LOCATION: 5
 57 <223> OTHER INFORMATION: Xaa is Ile or Val
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 61 1 5
 64 <210> SEQ ID NO: 3
 65 <211> LENGTH: 31
 66 <212> TYPE: DNA
 67 <213> ORGANISM: Mouse

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69 <220> FEATURE:
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 82 <223> OTHER INFORMATION: n is inosine
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 91 <213> ORGANISM: Mouse
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 94 <221> NAME/KEY: Unsure
 95 <222> LOCATION: 4
 96 <223> OTHER INFORMATION: Xaa is Asp or Glu
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 99 <221> NAME/KEY: Unsure
 100 <222> LOCATION: 5
 101 <223> OTHER INFORMATION: Xaa is Asn or Gln
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 105 1 5
 108 <210> SEQ ID NO: 5
 109 <211> LENGTH: 14
 110 <212> TYPE: PRT
 111 <213> ORGANISM: Mouse
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 119 <211> LENGTH: 583
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 123 <220> FEATURE:
 124 <221> NAME/KEY: CDS
 125 <222> LOCATION: (1)..(579)
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 130 1 5 10 15
 132 ttt gta ggt tat aag ctg agg cag aag ggt tat gtc tgt gga gct ggc 96
 133 Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly

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134          20          25          30
136 ccc ggg gag ggc cca gca gct gac ccg ctg cac caa gcc atg cgg gca 144
137 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
138          35          40          45
140 gct gga gat gag ttc gag acc cgc ttc cgg cgc acc ttc tct gat ctg 192
141 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
142          50          55          60
144 gcg gct cag ctg cat gtg acc cca ggc tca gcc cag caa cgc ttc acc 240
145 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
146          65          70          75          80
148 cag gtc tcc gac gaa ctt ttt caa ggg ggc ccc aac tgg ggc cgc ctt 288
149 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
150          85          90          95
152 gta gcc ttc ttt ctc ttt ggg gct gca ctg tgt gct gag agt gtc aac 336
153 Val Ala Phe Phe Leu Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
154          100          105          110
156 aag gag atg gaa cca ctg gtg gga caa gtg cag gag tgg atg gtg gcc 384
157 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
158          115          120          125
160 tac ctg gag acg cgg ctg gtc gac tgg atc cac agc agt ggg ggc tgg 432
161 Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp
162          130          135          140
164 gcg gag ttc aca gct cta tac ggg gac ggg gcc ctg gag gag gcg cgg 480
165 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
166          145          150          155          160
168 cgt ctg cgg gag ggg aac tgg gca tca gtg agg aca gtg ctg acg ggg 528
169 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
170          165          170          175
172 gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc 576
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174          180          185          190
176 aag tgaa 583
177 Lys
180 <210> SEQ ID NO: 7
181 <211> LENGTH: 193
182 <212> TYPE: PRT
183 <213> ORGANISM: HUMAN
185 <400> SEQUENCE: 7
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189 Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
190          20          25          30
192 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
193          35          40          45
195 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
196          50          55          60
198 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
199          65          70          75          80
201 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu

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202                               85          90          95
204 Val Ala Phe Phe Leu Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
205                               100          105          110
207 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
208                               115          120          125
210 Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp
211                               130          135          140
213 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
214                               145          150          155          160
216 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
217                               165          170          175
219 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
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226 <210> SEQ ID NO: 8
227 <211> LENGTH: 581
228 <212> TYPE: DNA
229 <213> ORGANISM: Mouse
231 <220> FEATURE:
232 <221> NAME/KEY: CDS
233 <222> LOCATION: (1)..(579)
235 <400> SEQUENCE: 8
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237 Met Pro Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp
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240 ttt gta ggc tat agg ctg agg cag aag ggt tat gtc tgt gga gct ggg 96
241 Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
242 20 25 30
244 cct ggg gaa ggc cca gcc gcc gac ccg ctg cac caa gcc atg cgg gct 144
245 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
246 35 40 45
248 gct gga gac gag ttt gag acc cgt ttc cgc cgc acc ttc tct gac ctg 192
249 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
250 50 55 60
252 gcc gct cag cta cac gtg acc cca ggc tca gcc cag caa cgc ttc acc 240
253 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
254 65 70 75 80
256 cag gtt tcc gac gaa ctt ttc caa ggg ggc cct aac tgg ggc cgt ctt 288
257 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
258 85 90 95
260 gtg gca ttc ttt gtc ttt ggg gct gcc ctg tgt gct gag agt gtc aac 336
261 Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
262 100 105 110
264 aaa gaa atg gag cct ttg gtg gga caa gtc cag gat tgg atc gtg gcc 384
265 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala
266 115 120 125
268 tac ctg gag aca cgt ctg gct gac tgg atc cac agc agt ggc ggc tgg 432
269 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
270 130 135 140

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272 gcg gac ttc aca gct cta tac ggg gac ggg gcc ctg gag gac gca cgg 480
273 Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg
274 145 150 155 160
276 cgt ctg cgg gag ggc aac tgg gca tga gtg agc aca gtg gtg acg ggg 528
277 Arg Leu Arg Glu Gly Asn Trp Ala Val Ser Thr Val Val Thr Gly Ala
278 165 170 175
280 gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc 576
281 Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser Lys
282 180 185 190
284 aag tg 581
288 <210> SEQ ID NO: 9
289 <211> LENGTH: 192
290 <212> TYPE: PRT
291 <213> ORGANISM: Mouse
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299 35 40 45
300 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
301 50 55 60
302 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
303 65 70 75 80
304 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
305 85 90 95
306 Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
307 100 105 110
308 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala
309 115 120 125
310 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
311 130 135 140
312 Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg
313 145 150 155 160
314 Arg Leu Arg Glu Gly Asn Trp Ala Val Ser Thr Val Val Thr Gly
315 165 170 175
316 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
317 180 185 190
318 Lys

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VERIFICATION SUMMARY
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Input Set : A:\11686.seq2
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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4